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=> s ((in silico) and identif?)/clm
           220 IN SILICO/CLM
                 ((SILICO)/CLM)
        113642 IDENTIF?/CLM
L1          11 ((IN SILICO) AND IDENTIF?)/CLM

=> d bib,kwic 1-11

L1   ANSWER 1 OF 11  USPATFULL
AN     2002:191545  USPATFULL
TI     Automated identification of peptides
IN     Townsend, Robert Reid, Oxford, UNITED KINGDOM
       Robinson, Andrew William, Saskatoon, CANADA
PI     US 2002102610      A1   20020801
AI     US 2001-950313     A1   20010910 (9)
PRAI   GB 2000-22136       20000908
       US 2000-232273P     20000913 (60)
DT     Utility
FS     APPLICATION
LREP   PENNIE AND EDMONDS, 1155 AVENUE OF THE AMERICAS, NEW YORK, NY, 100362711
CLMN   Number of Claims: 6
ECL    Exemplary Claim: 1
DRWN   14 Drawing Page(s)
LN.CNT 2657
CLM    What is claimed is:
       1. A computer-based method for determining whether or not a first
       peptide sequence database obtained by in silico tryptic
       digestion of a second peptide sequence database contains one or more
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peptide sequences that correspond to an experimental peptide. . . . in the peak list according to one or more matching criteria, the back-read comprising: (i) for each candidate sequence, (1) **identifying** one or more amino acids flanking the search sequence (X) that is included in the candidate sequence; (2) generating a list of theoretical m/z values of at least one suite of ions for the **identified** flanking amino acids; (3) comparing the theoretical m/z values or corresponding assigned mass values with observed values in the first. . . matching criteria, wherein upon satisfaction of the matching criteria, the candidate sequences, if any, that satisfy the matching criteria are **identified** as corresponding sequences.

L1 ANSWER 2 OF 11 USPATFULL
AN 2002:191512 USPATFULL
TI Nucleotide incorporating enzymes
IN Raillard, Sun Ai, Mountain View, CA, UNITED STATES
Welch, Mark, Fremont, CA, UNITED STATES
Ness, Jon, Sunnyvale, CA, UNITED STATES
PI US 2002102577 A1 20020801
AI US 2001-920452 A1 20010731 (9)
PRAI US 2000-244764P 20001031 (60)
US 2000-222056P 20000731 (60)
DT Utility
FS APPLICATION
LREP LAW OFFICES OF JONATHAN ALAN QUINE, P O BOX 458, ALAMEDA, CA, 94501
CLMN Number of Claims: 87
ECL Exemplary Claim: 1
DRWN 4 Drawing Page(s)
LN.CNT 2833
CLM What is claimed is:
. . . nucleic acid segments encode all or part of one or more parental nucleotide incorporating enzymes or a homologue thereof; (b) **identifying** at least one non-natural or rare nucleotide analogue to be incorporated by the nucleotide incorporating enzyme, which non-natural or rare. . . the plurality of nucleic acid segments, thereby producing a library of nucleic acids encoding nucleotide incorporating enzyme variants; and (d) **identifying** at least one nucleotide incorporating enzyme variant that incorporates the non-natural or rare nucleotide analogue at least about 10% as. . .
5. The method of claim 1, comprising **identifying** a nucleotide analogue selected from the group consisting of: a nucleotide derivatized with a functional group, a nucleotide derivatized with. . .
. . . the plurality of nucleic acid segments by recombining the plurality of nucleic acid segments in vitro, in vivo, or in **silico**.

. . . The method of claim 28, comprising recursively recombining the plurality of nucleic acid segments in vitro, in vivo, or in **silico**.

39. The method of claim 1, comprising **identifying** the at least one nucleotide incorporating enzyme variant that incorporates the non-natural or rare nucleotide analogue by mass spectroscopy.

40. The method of claim 1, comprising **identifying** the at least one nucleotide incorporating enzyme variant that incorporates the non-natural or rare nucleotide analogue by one or more. . .
41. The method of claim 1, comprising **identifying** the at least one nucleotide incorporating enzyme by: (i) transforming the library of nucleic acids into a population of host. . . the at least one essential naturally occurring nucleotide of the first medium and comprises the non-natural or rare nucleotide analogue **identified** in step (b); and (iii) **identifying** at least one surviving transformed host cell, thereby **identifying** a nucleic acid

encoding a nucleotide incorporating enzyme variant, which nucleotide incorporating enzyme variant incorporates the non-natural or rare nucleotide. . .

42. The method of claim 1, comprising **identifying** the at least one nucleotide incorporating enzyme variant in a high throughput assay format.

. . . nucleotide incorporating enzyme deficient bacterial host cells; (ii) growing the transformed bacterial host cells at the non-permissive temperature; and (iii) **identifying** one or more transformed bacterial host cells capable of growth at the non-permissive temperature, thereby **identifying** one or more members of the library of nucleic acids that encodes a functional nucleotide incorporating enzyme.

44. The method of claim 1, further comprising **identifying** at least one nucleotide incorporating enzyme variant with at least one additional desired property.

46. The method of claim 44, comprising **identifying** at least one nucleotide incorporating enzyme variant by simultaneously screening for incorporation of the non-natural or rare nucleotide analogue and. . .

. . . nucleic acid segments encode all or part of one or more parental nucleotide incorporating enzymes or a homologue thereof; (b) **identifying** at least one non-natural or rare nucleotide analogue to be incorporated by the nucleotide incorporating enzyme, which non-natural or rare. . . the plurality of nucleic acid segments, thereby producing a library of nucleic acids encoding nucleotide incorporating enzyme variants; and (d) **identifying** at least one nucleotide incorporating enzyme variant that incorporates the non-natural or rare nucleotide analogue at least about 10 fold. . .

54. The method of claim 47, wherein the at least one nucleotide incorporating enzyme variant **identified** in step (d) incorporates the non-natural or rare nucleotide analogue at least about 20 fold more efficiently than at least. . .

55. The method of claim 47, wherein the at least one nucleotide incorporating enzyme variant **identified** in step (d) incorporates the non-natural or rare nucleotide analogue at least about 50 fold more efficiently than at least. . .

56. The method of claim 47, wherein the at least one nucleotide incorporating enzyme variant **identified** in step (d) incorporates the non-natural or rare nucleotide analogue at least about 100 fold more efficiently than at least. . .

. . . comprising extending a plurality of nucleic acid segments annealed to a single stranded template using the nucleotide incorporating enzyme variant **identified** in step (d).

. . . The method of claim 1 or 47, further comprising performing at least one PCR using the nucleotide incorporating enzyme variant **identified** in step (d).

. . . method of claim 1 or 47, further comprising performing at least one sequencing reaction using the nucleotide incorporating enzyme variant **identified** in step (d).

. . . the plurality of nucleic acid segments, thereby producing a library of nucleic acids encoding nucleotide incorporating enzyme variants; and (c) **identifying** at least one nucleotide incorporating enzyme variant that efficiently polymerizes a polynucleotide in a template dependent manner in the presence. . .

67. The method of claim 60, wherein the at least one nucleotide incorporating enzyme **identified** in step (c) is **identified** in a high throughput assay.

68. The method of claim 60, wherein the at least one nucleotide incorporating enzyme **identified** in step (c) comprises a thermostable enzyme.

69. The method of claim 60, wherein the at least one nucleotide incorporating enzyme **identified** in step (c) comprises an enzyme that is capable of incorporating dUTP.

70. The method of claim 60, wherein the at least one nucleotide incorporating enzyme **identified** in step (c) comprises an enzyme that is incorporates dUTP at least as efficiently as a nucleotide incorporating enzyme selected. . .

71. The method of claim 60, wherein the at least one nucleotide incorporating enzyme **identified** in step (c) is active in a reaction mixture comprising at least about 20% blood.

72. The method of claim 60, wherein the at least one nucleotide incorporating enzyme **identified** in step (c) is active in a reaction mixture comprising at least about 50% plasma.

73. The method of claim 60, wherein the at least one nucleotide incorporating enzyme **identified** in step (c) is active in a reaction mixture comprising at least about 50% urine.

86. A method for **identifying** a nucleotide incorporating enzyme with having a desired property, the method comprising: a) providing a plurality of partially duplexed oligonucleotides. . .

L1 ANSWER 3 OF 11 USPATFULL
AN 2002:141115 USPATFULL
TI Molecular breeding of transposable elements
IN delCardayre, Stephen, Belmont, CA, UNITED STATES
Patnaik, Ranjan, San Jose, CA, UNITED STATES
Patten, Phillip, Menlo Park, CA, UNITED STATES
Tobin, Matthew, San Jose, CA, UNITED STATES
Ness, Jon E., Sunnyvale, CA, UNITED STATES
Cox, Anthony, Mountain View, CA, UNITED STATES
Giver, Lorraine J., Santa Clara, CA, UNITED STATES
McBride, Kevin, Davis, CA, UNITED STATES
Zahn, Kenneth, Redwood City, CA, UNITED STATES
PI US 2002072097 A1 20020613
AI US 2001-899814 A1 20010705 (9)
PRAI US 2000-216798P 20000707 (60)
DT Utility
FS APPLICATION
LREP LAW OFFICES OF JONATHAN ALAN QUINE, P O BOX 458, ALAMEDA, CA, 94501
CLMN Number of Claims: 115
ECL Exemplary Claim: 1
DRWN 9 Drawing Page(s)
LN.CNT 2871
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
CLM What is claimed is:
. . . element; ii) recombining the polynucleotide segments one or more times, thereby producing a library of recombinant transposable element components; iii) **identifying** at least one recombinant transposable element component with a desired property; iv) optionally repeating steps (i) through (iii) at least. . .

12. The method of claim 1, comprising recombining the polynucleotide segments in vitro, in vivo, or in **silico**.

14. The method of claim 1, wherein the **identifying** of step (iii) comprises screening or selecting at least one transposable element with a desired property.

15. The method of claim 14, comprising **identifying** at least one transposable element that mediates transposition in vitro with greater efficiency when compared to a parental transposable element,. . . (c) a target polynucleotide incubating the plurality of in vitro transposition reactions under conditions permissive for in vitro transposition; and **identifying** at least one in vitro transposition reaction that occurs with greater efficiency than an in vitro transposition reaction mediated by. . .
17. The method of claim 14, comprising **identifying** at least one transposable element that transposes with increased efficiency in a specified host cell when compared with a wild. . .
. . . ii) recombining the polynucleotide segments one or more times, thereby producing a library of recombinant polynucleotides encoding variant transposases; iii) **identifying** at least one recombinant polynucleotide encoding a transposase that efficiently catalyzes in vitro transposition.

53. The method of claim 52, comprising **identifying** the at least one recombinant polynucleotide encoding a transposase that efficiently catalyzes in vitro transposition by: a) providing a plurality. . . target polynucleotide; b) incubating the plurality of in vitro transposition reactions under conditions permissive for in vitro transposition; and c) **identifying** at least one in vitro transposition reaction that occurs with greater efficiency than an in vitro transposition reaction mediated by. . .
60. The method of claim 57, further comprising **identifying** at least one altered subject nucleic acid.

. . . 68, further comprising, introducing the library of recombinant nucleic acids or a subportion thereof into a population of cells and **identifying** at least one cell with a desired property.

81. A method for **identifying** a chromosomal locus, which chromosomal locus exhibits a desired level of gene expression, the method comprising: i) transfecting a plurality. . . or selectable marker; (e) a polynucleotide encoding a second screenable or selectable marker; and (f) a second inverted repeat; ii) **identifying** at least one host cell that expresses a sufficient level of at least one selectable marker, which selectable marker is encoded by the first or second visible or selectable marker, to survive selection, thereby **identifying** at least one host cell that has integrated the vector into a chromosome; and iii) **identifying** at least one host cell expressing at least one screenable or selectable marker at a desired level, thereby **identifying** a chromosomal locus exhibiting a desired level of gene expression.

83. The method of claim 81, further comprising integrating a polynucleotide sequence of interest into the **identified** chromosomal locus to generate at least one integrant.

84. The method of claim 82, further comprising **identifying** at least one integrant with a desired level of expression.

L1 ANSWER 4 OF 11 USPATFULL
AN 2002:112517 USPATFULL
TI Short shared nucleotide sequences
IN Ananiev, Evgueni V., Johnston, IA, UNITED STATES
PI US 2002058252 A1 20020516
AI US 2000-730468 A1 20001204 (9)
PRAI US 1999-169157P 19991206 (60)
DT Utility
FS APPLICATION

LREP PIONEER HI-BRED INTERNATIONAL INC., 7100 N.W. 62ND AVENUE, P.O. BOX 1000, JOHNSTON, IA, 50131
CLMN Number of Claims: 21
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 1971
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
CLM What is claimed is:

1. A method of **identifying** differentiating subsets of short shared nucleotide sequences or of differentiating at least one target nucleic acid sequence from other members. . . comprises a nucleic acid subsequence that is common to at least two members of the first nucleic acid population; and, **identifying** differentiating subsets of the set of short shared nucleotide sequences, wherein each differentiating subset comprises a subset of the set. . .

13. The method of claim 3, wherein at least one step occurs in vitro or in **silico**.

14. The method of claim 3, wherein the hybridizing step comprise; concomitantly hybridizing at least one competitor differentiating nucleic acid. . . nucleic acid probes, thereby minimizing non-specific cross-hybridization; or, wherein the target nucleic acid sequence is detected at least twice by **identifying** members of the first or the second nucleic acid population that hybridize the same set of differentiating nucleic acid probes; or, wherein the target nucleic acid sequence is detected at least twice by **identifying** members of the first or the second nucleic acid population that hybridize to the same set of differentiating nucleic acid. . .

L1 ANSWER 5 OF 11 USPATFULL
AN 2002:85135 USPATFULL
TI Gene recombination and hybrid protein development
IN Wang, Zhen-Gang, Pasadena, CA, UNITED STATES
Voigt, Christopher A., Pasadena, CA, UNITED STATES
Mayo, Stephen L., Pasadena, CA, UNITED STATES
Arnold, Frances H., Pasadena, CA, UNITED STATES
PI US 2002045175 A1 20020418
AI US 2001-863765 A1 20010523 (9)
PRAI US 2000-207048P 20000523 (60)
US 2000-235960P 20000927 (60)
US 2001-283567P 20010413 (60)
DT Utility
FS APPLICATION
LREP DARBY & DARBY, 805 THIRD AVENUE, 27TH FLR., NEW YORK, NY, 10022
CLMN Number of Claims: 151
ECL Exemplary Claim: 1
DRWN 25 Drawing Page(s)
LN.CNT 3895
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
CLM What is claimed is:

. . . polymer sequence, for recombination with one or more second biopolymers each having its own second polymer sequence, which method comprises: **identifying** coupling interactions between pairs of residues in the first polymer sequence; generating a plurality of data structures, each data structure. . . crossover disruption related to the number of coupling interactions disrupted in the crossover mutant represented by the data structure; and **identifying**, among the plurality of data structures, a particular data structure having a crossover disruption below a threshold, wherein the crossover location of the crossover mutant represented by the particular data structure is the **identified** crossover location.

4. A method of claim 1, wherein coupling interactions are **identified** by use of a coupling matrix.

6. A method of claim 1, wherein coupling interactions are **identified** by a determination of a conformational energy between residues.

7. A method of claim 1, wherein coupling interactions are **identified** by a determination of interatomic distances between residues.

10. A method of claim 2, wherein coupling interactions are **identified** by a conformational energy between residues above a threshold.

. . . method of claim 1, wherein the generation of crossover mutants comprises: the sequence alignment of a plurality of biopolymers; the **identification** of possible cut points in the biopolymer based upon regions of sequence identity **identified** by the sequence alignment; and the generation of single crossover mutants based upon the **identified** possible cut points.

. . . crossover disruption, fragment size, starting number of parents; and the generation of a plurality of data structures based upon the **identified** possible crossover locations.

24. A method of claim 19, wherein the generation of the plurality of data structures based upon **identified** cut points comprises: cutting the biopolymers in into biopolymer fragments by randomly assigning cut points with a set probability; randomly choosing one of the biopolymer fragments as a starting parent; randomly **identifying** another biopolymer fragment from the total pool of the biopolymer fragments; ligating the **identified** biopolymer fragment to the parent fragment, if the **identified** fragment has a sequence identity cut-point at the end of the fragment; and repeating the randomly **identifying** step until the data structure, representing the crossover mutant is the desired length.

. . . A method for directed evolution of a polymer, which method comprises steps of: providing a plurality of parent polymer sequences; **identifying** crossover locations in the parent polymer sequences for recombination according to claim 1; generating one or more mutant polymer sequences utilizing recombinatory techniques targeted at the **identified** crossover locations on the parent polymer sequences; screening the one or more mutant sequences for the one or more properties of interest; and selecting at least one mutant sequence where one or more properties of interest are **identified**.

41. A method for producing hybrid polymers from two or more parent polymers comprising the steps of: **identifying** structural domains of at least one parent polymer; organizing **identified** domains into schema; calculating a schema disruption profile; selecting at least one crossover location based on the schema disruption profile;. . .
42. A method of claim 41, wherein parent polymers are recombined in **silico**, in vitro, in vivo, or in any combination thereof.

43. A method of claim 41, wherein parent polymers are recombined in **silico** to produce at least one candidate hybrid polymer.

. . . of claim 51, wherein the sequence space of a directed evolution experiment is reduced based on a library of in **silico** candidate hybrid candidate sequences.

. . . 71. A method for producing a library of hybrid polymers comprising the steps of: choosing two or more parent polymers;

**identifying** structural domains of at least one parent polymer; organizing **identified** domains into schema; calculating a schema disruption profile; selecting crossover locations based on the schema disruption profile; recombining two or. . .
73. A method of claim 71, wherein recombining steps are performed in **silico**.

83. A method of claim 41, wherein schema comprise domains **identified** according to sequence alignments between two or more parent polymers.

84. A method of claim 71, wherein schema comprise domains **identified** according to sequence alignments between two or more parent polymers.

. . . 41, further comprising the steps of generating a coupling matrix and using the matrix in at least one of the **identifying**, organizing, calculating, and selecting steps.

. . . 71, further comprising the steps of generating a coupling matrix and using the matrix in at least one of the **identifying**, organizing, calculating, and selecting steps.

96. A method of claim 41, wherein domains are **identified** based on sequence information for at least one parent polymer.

97. A method of claim 71, wherein domains are **identified** based on sequence information for at least one parent polymer.

98. A method of claim 41, wherein domains are **identified** based on a crystal structure for at least one parent polymer.

99. A method of claim 71, wherein domains are **identified** based on a crystal structure for at least one parent polymer.

. . . obtaining structural information for at least one parent polymer; evaluating coupling interactions between polymer residues based on the structural information; **identifying** domains based on the determined coupling interactions; calculating the crossover disruption of the **identified** domains to produce a disruption profile; applying a predetermined threshold disruption to each domain of the disruption profile; at least. . . of, accepting domains which satisfy the threshold and rejecting domains which do not satisfy the threshold; repeating at least the **identifying**, calculating and applying steps until each **identified** domain is accepted or rejected; designating the accepted or rejected domains as disruptive; selecting crossover regions from domains that are. . .
102. A method of claim 101, wherein the step of **identifying** domains comprises determining the polymer residues which belong to each domain, and the step of selecting crossover regions comprises specifying. . .
. . . between parents, and the method further comprises: obtaining sequence information for the parent polymers; aligning the obtained sequence information; and **identifying** cut points within aligned regions of the parent sequences.

110. A method of claim 109, where the step of **identifying** cut points comprises selecting cut points having a relatively low crossover disruption, and the step of specifying a set of. . .

L1 ANSWER 6 OF 11 USPATFULL
AN 2002:61901 USPATFULL
TI Evolution of plant disease response plant pathways to enable the development of based biological sensors and to develop novel disease

resistance strategies
IN Lassner, Michael, Foster City, CA, UNITED STATES
English, James, Burlingame, CA, UNITED STATES
Wu, Gusui, Davis, CA, UNITED STATES
PI US 2002035739 A1 20020321
AI US 2001-849452 A1 20010504 (9)
PRAI US 2000-202233P 20000505 (60)
DT Utility
FS APPLICATION
LREP LAW OFFICES OF JONATHAN ALAN QUINE, P O BOX 458, ALAMEDA, CA, 94501
CLMN Number of Claims: 127
ECL Exemplary Claim: 1
DRWN 1 Drawing Page(s)
LN.CNT 2493
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
CLM What is claimed is:

1. A method for **identifying** a plant disease resistance gene with a specified characteristic, the method comprising: (a) providing a plurality of disease resistance (R). . . plant cell to an elicitor of a plant defense response; and (e) detecting at least one plant defense response, thereby **identifying** a plant disease resistance (R) gene with a specified characteristic.

. . . 6. The method of claim 1, comprising recombining the population of R gene segments in vivo, in vitro or in **silico**.

39. The method of claim 37, detecting at least one plant defense response, thereby **identifying** an elicitor with a desired property.

45. A method for **identifying** an elicitor of a plant defense response with a desired property, the method comprising: (a) providing a plurality of nucleic. . . of the library of recombinant nucleic acids of step (b); and (e) detecting at least one plant defense response, thereby **identifying** at least one elicitor with a desired property.

49. The method of claim 45, comprising recombining the plurality of nucleic acids in vivo, in vitro or in **silico**.

73. A method for **identifying** a functional interaction between a plant disease resistance gene and an elicitor, the method comprising: (i) introducing a first viral. . . are cytoplasmically expressed in the at least one plant cell; and (ii) detecting at least one plant defense response, thereby **identifying** a functional interaction between the R gene and the elicitor.

83. A method for **identifying** a functional interaction between a plant disease resistance gene and an elicitor, the method comprising: (i) exposing at least one. . . plant defense response and a plant disease resistance (R) gene; and (ii) detecting at least one plant defense response, thereby **identifying** a functional interaction between the R gene and the elicitor.

. . . recombinant RNA viral vectors; (c) optionally recovering at least one recombinant viral vector and repeating steps (a) and (b); (d) **identifying** at least one RNA viral vector comprising a gene with a desired property.

124. The method of claim 105, comprising **identifying** the at least one RNA viral vector comprising a gene with a desired property by selection or screening.

. . . infection in a plant, which first and second viral vectors have

complementary mutations in genes essential for systemic infection, and **identifying** at least one recombinant RNA viral vector by selecting or screening for RNA viral vectors capable of systemic infection.

L1 ANSWER 7 OF 11 USPATFULL
AN 2002:48730 USPATFULL
TI IDENTIFICATION OF GENETIC TARGETS FOR MODULATION BY OLIGONUCLEOTIDES AND GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
IN COWSERT, LEX M., CARLSBAD, CA, UNITED STATES
BAKER, BRENDA F., CARLSBAD, CA, UNITED STATES
MCNEIL, JOHN, LA JOLLA, CA, UNITED STATES
FREIER, SUSAN M., DIEGO, CA, UNITED STATES
SASMOR, HENRI M., ENCINITAS, CA, UNITED STATES
PI US 2002028923 A1 20020307
AI US 1998-67638 A1 19980428 (9)
DT Utility
FS APPLICATION
LREP JOHN W CADWELL, WOODCOCK WASHBURN KURTZ MACKIEWICZ, & NORRIS, ONE LIBERTY PLACE 46TH FLOOR, PHILADELPHIA, PA, 19103
CLMN Number of Claims: 46
ECL Exemplary Claim: 1
DRWN 24 Drawing Page(s)
LN.CNT 4226
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
CLM What is claimed is:

. . . of compounds that modulate the expression of a target nucleic acid sequence comprising generating a library of nucleobase sequences in **silico** according to defined criteria.

. . . method of generating a set of compounds that modulate the expression of a target nucleic acid sequence comprising evaluating in **silico** a plurality of virtual oligonucleotides according to defined criteria.

. . . of compounds that modulate the expression of a target nucleic acid sequence comprising generating a library of nucleobase sequences in **silico** according to defined criteria and evaluating in **silico** a plurality of virtual oligonucleotides having said nucleobase sequences according to defined criteria.

. . . method of generating a set of compounds that modulate the expression of a target nucleic acid sequence comprising evaluating in **silico** a plurality of virtual oligonucleotides according to defined criteria and robotically synthesizing a plurality of oligonucleotide compounds corresponding to said. . .

. . . method of generating a set of compounds that modulate the expression of a target nucleic acid sequence comprising evaluating in **silico** a plurality of virtual oligonucleotides according to defined criteria and robotically assaying a plurality of oligonucleotide compounds corresponding to said. . .

. . . of compounds that modulate the expression of a target nucleic acid sequence comprising generating a library of nucleobase sequences in **silico** according to defined criteria and robotically synthesizing a plurality of oligonucleotide compounds having said nucleobase sequences.

. . . of compounds that modulate the expression of a target nucleic acid sequence comprising generating a library of nucleobase sequences in **silico** according to defined criteria and robotically assaying a plurality of oligonucleotide compounds having said nucleobase sequences for one or more. . .

. . . the expression of a target nucleic acid sequence, comprising the

steps of: (a) generating a library of nucleobase sequences in **silico** according to defined criteria; (b) evaluating in **silico** a plurality of virtual oligonucleotides having the nucleobase sequences of (a) according to defined criteria; and (c) robotically synthesizing a. . .

. . . the expression of a target nucleic acid sequence, comprising the steps of: (a) generating a library of nucleobase sequences in **silico** according to defined criteria; (b) evaluating in **silico** a plurality of virtual oligonucleotides having the nucleobase sequences of (a) according to defined criteria; and (c) robotically assaying a. . .

. . . the expression of a target nucleic acid sequence, comprising the steps of: (a) generating a library of nucleobase sequences in **silico** according to defined criteria; (b) robotically synthesizing a plurality of oligonucleotide compounds; and (c) robotically assaying a plurality of oligonucleotide. . .

. . . set of compounds that modulate the expression of a target nucleic acid sequence, comprising the steps of: (a) evaluating in **silico** a plurality of virtual oligonucleotides according to defined criteria; (b) robotically synthesizing a plurality of oligonucleotide compounds; and (c) robotically. . .

. . . the expression of a target nucleic acid sequence, comprising the steps of: (a) generating a library of nucleobase sequences in **silico** according to defined criteria; (b) evaluating in **silico** a plurality of virtual oligonucleotides having the nucleobase sequences of (a) according to defined criteria; (c) robotically synthesizing a plurality. . .

. . . the expression of a target nucleic acid sequence, comprising the steps of: (a) generating a library of nucleobase sequences in **silico** according to defined criteria; (b) choosing an oligonucleotide chemistry; (c) robotically synthesizing a set of oligonucleotide compounds having said nucleobase. . .

. . . the expression of a target nucleic acid sequence, comprising the steps of: (a) generating a library of nucleobase sequences in **silico** according to defined criteria; (b) choosing an oligonucleotide chemistry; (c) evaluating in **silico** a plurality of virtual oligonucleotides having the nucleobase sequences of (a) and the oligonucleotide chemistry of (b) according to defined. . .

21. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation comprising generating a library of antisense nucleobase sequences in **silico** according to defined criteria.

22. A method of generating a set of compounds that modulate the expression of a target nucleic acid sequence comprising evaluating in **silico** a plurality of virtual oligonucleotides according to defined criteria.

23. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation comprising robotically synthesizing a plurality of antisense compounds.

24. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation comprising robotically assaying a plurality of antisense compounds for one. . .

25. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation comprising generating a library of nucleobase sequences in **silico** according to defined criteria and evaluating in **silico** a plurality of virtual oligonucleotides having said nucleobase sequences according to defined criteria.

26. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation comprising evaluating in **silico**

a plurality of virtual oligonucleotides according to defined criteria and robotically synthesizing a plurality of oligonucleotide compounds.

27. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation comprising evaluating in **silico** a plurality of virtual oligonucleotides according to defined criteria and robotically assaying a plurality of oligonucleotide compounds for one or. . .

28. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation comprising generating a library of nucleobase sequences in **silico** according to defined criteria and robotically synthesizing a plurality of oligonucleotide compounds having said nucleobase sequences.

29. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation comprising robotically synthesizing a plurality of oligonucleotide compounds and robotically. . .

30. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation comprising generating a library of nucleobase sequences in **silico** according to defined criteria and robotically assaying a plurality of oligonucleotide compounds having said nucleobase sequences for one or more. . .

31. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation comprising the steps of: (a) generating a library of nucleobase sequences in **silico** according to defined criteria; (b) evaluating in **silico** a plurality of virtual oligonucleotides having the nucleobase sequences of (a) according to defined criteria; and (c) robotically synthesizing a. . .

32. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation, comprising the steps of: (a) generating a library of nucleobase sequences in **silico** according to defined criteria; (b) evaluating in silica a plurality of virtual oligonucleotides having the nucleobase sequences of (a) according. . .

33. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation, comprising the steps of: (a) generating a library of nucleobase. . .

34. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation, comprising the steps of: (a) evaluating in **silico** a plurality of virtual oligonucleotides according to defined criteria; (b) robotically synthesizing a plurality of oligonucleotide compounds; and (c) robotically. . .

35. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation, comprising the steps of: (a) generating a library of nucleobase sequences in **silico** according to defined criteria; (b) evaluating in **silico** a plurality of virtual oligonucleotides having the nucleobase sequences of (a) according to defined criteria; (c) robotically synthesizing a plurality. . .

36. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation, comprising the steps of: (a) generating a library of nucleobase sequences in **silico** according to defined criteria; (b) choosing an oligonucleotide chemistry; (c) robotically synthesizing a set of oligonucleotide compounds having said nucleobase. . .

37. A method of **identifying** one or more nucleic acid sequences amenable to antisense modulation, comprising the steps of: (a) generating a library of nucleobase sequences in **silico** according to defined criteria; (b) choosing an oligonucleotide chemistry; (c) evaluating in **silico** a plurality of virtual oligonucleotides having the nucleobase sequences of (a) according to defined criteria, and selecting those having preferred. . .

41. A computer formatted medium comprising computer readable

instructions for **identifying** active compounds.

43. A computer formatted medium comprising computer readable instructions for performing a method of **identifying** one or more nucleic acid sequences amenable to antisense modulation.

. . . nucleic acid sequences amenable to antisense modulation in computer readable form, wherein said one or more nucleic acid sequences is **identified** according to the method of any one of claims 21, 22 or 24-40.

L1 ANSWER 8 OF 11 USPATFULL
AN 2002:32167 USPATFULL
TI In silico screening
IN Klinck, Roscoe, Cambridge, UNITED KINGDOM
Walker, Stephen, Willinghan Cambs, UNITED KINGDOM
Afshar, Mohammad, Cambridge, UNITED KINGDOM
Collier, Adam, Burwell Cambs, UNITED KINGDOM
Aboul-ela, Fareed, Cambridge, UNITED KINGDOM
Westhof, Eric, Strasbourg, FRANCE
PI US 2002018988 A1 20020214
AI US 2001-843135 A1 20010426 (9)
PRAI GB 2000-10173 20000426
US 2000-199773P 20000426 (60)
DT Utility
FS APPLICATION
LREP PALMER & DODGE, LLP, ONE BEACON STREET, BOSTON, MA, 02108-3190
CLMN Number of Claims: 14
ECL Exemplary Claim: 1
DRWN 8 Drawing Page(s)
LN.CNT 667
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
CLM What is claimed is:
1. An in **silico** method for **identifying** a compound that interacts with sub-domain IIId of the hepatitis C virus IRES, comprising the steps of: (a) providing atomic. . .
5. The method of claim 4, wherein the de novo compound design involves (i) the **identification** of functional groups or small molecule fragments which can interact with sites in the binding surface of sub-domain IIId, and. . .
10. The method of claim 1, comprising the additional steps, following step (b), of: (c) providing a compound **identified** by said molecular modelling techniques; and (d) contacting said compound with the HCV IRES and detecting the interaction between them.
. . .
11. A compound **identified** using the method of claim 1.

14. An assay for displacement from a fragment of the HCV IRES, wherein the assay utilises a reporter molecule **identified** using the method of claim 8 or claim 9.

L1 ANSWER 9 OF 11 USPATFULL
AN 2001:199911 USPATFULL
TI Integrated systems and methods for diversity generation and screening
IN Bass, Steven H., Hillsborough, CA, United States
Davis, S. Christopher, San Francisco, CA, United States
Patten, Phillip A., Menlo Park, CA, United States
Tobin, Matthew, San Jose, CA, United States
Minshull, Jeremy, Menlo Park, CA, United States
Welch, Mark, Fremont, CA, United States
Gustafsson, Claes, Belmont, CA, United States
Carr, Brian, Fremont, CA, United States

Jenne, Stephane, Burlingame, CA, United States
Raillard, Sun Ai, Mountain View, CA, United States
Crameri, Andreas, Reinach, Switzerland
Stemmer, Willem P.C., Los Gatos, CA, United States
Emig, Robin, Redwood City, CA, United States
Longchamp, Pascal, East Palo Alto, CA, United States
Goldman, Stanley, Walnut Creek, CA, United States
Giver, Lorraine J., Santa Clara, CA, United States
Affholter, Joseph A., Lake Village Zephyr Cove, NV, United States

PA Maxygen, Inc., Redwood City, CA, United States, 94063 (U.S. corporation)
PI US 2001039014 A1 20011108
AI US 2001-760010 A1 20010110 (9)
PRAI US 2000-175551P 20000111 (60)
US 2000-213947P 20000623 (60)
DT Utility
FS APPLICATION
LREP LAW OFFICES OF JONATHAN ALAN QUINE, P O BOX 458, ALAMEDA, CA, 94501
CLMN Number of Claims: 299
ECL Exemplary Claim: 1
DRWN 40 Drawing Page(s)
LN.CNT 8292
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
CLM What is claimed is:

23. The device or integrated system of claim 14, or 20, wherein the nucleic acid shuffling module comprises an **identification** portion, which **identification** portion **identifies** one or more nucleic acid portion or subportion.

28. The device or integrated system of claim 25, wherein the nucleic acid shuffling module separates, **identifies**, purifies or immobilizes the resulting elongated nucleic acid.

. . . reaction mixtures produces an array of reaction mixture products, the device or integrated system further comprising one or more product **identification** or purification modules, which product **identification** modules **identify** one or more members of the array of reaction products.

65. The device or integrated system of claim 64, wherein the product **identification** or purification modules comprise one or more of: a gel, a polymeric solution, a liposome, a microemulsion, a microdroplet, an. . .

. . . system of claim 64, wherein the one or more reaction product array members are moved into proximity to the product **identification** module, or wherein the product **identification** module performs an xyz translation, thereby moving the product **identification** module proximal to the array of reaction products.

. . . system of claim 66, wherein the one or more reaction product array members are flowed into proximity to the product **identification** module, wherein an in-line purification system purifies the one or more reaction product array members from associated materials.

73. The device or integrated system of claim 64, the product **identification** or purification modules comprising one or more of: a protein detector, or protein purification means.

74. The device or integrated system of claim 64, the product **identification** or purification modules comprising an instruction set for discriminating between members of the array of reaction products based upon one. . .

. . . integrated system of claim 64, the device or integrated system further comprising an array correspondence module, which array correspondence module **identifies**, determines or records the

location of an **identified** product in the array of reaction mixture products which is **identified** by the one or more product **identification** modules, or which array correspondence module determines or records the location of at least a first nucleic acid member of. . .

. . . module selects at least the first member for further recombination, which selection is based upon the location of a product **identified** by the product **identification** modules.

140. The method of claim 139, further comprising separating, **identifying**, cloning or purifying the resulting elongated DNAs.

. . . The method of claim 153, comprising moving the one or more reaction product array members into proximity to a product **identification** module, or moving a product **identification** module into proximity to the reaction product array members.

. . . method of claim 153, wherein the one or more reaction product array members are flowed into proximity to a product **identification** module, the method further comprising in-line purification of the one or more reaction product array members.

. . . The method of claim 203, further comprising selecting the physical or logical array of polypeptides for a desired property, thereby **identifying** one or more selected member of the physical or logical array of polypeptides which has a desired property, thereby **identifying** one or more selected member of the amplified physical or logical array of recombinant nucleic acids that encodes the one. . .

. . . or logical array of recombinant nucleic acids with one or more additional nucleic acids, in vivo, in vitro or in **silico**.

. . . nucleic acids comprise a related population of shuffled nucleic acids and a PCR primer binding region, the method further comprising **identifying** one or more target first nucleic acid by proximity to the moieties which are bound to the one or more. . .

278. The method of claim 247, further comprising **identifying** at least one substantially full-length heterolog with a desired property.

279. The method of claim 278, comprising **identifying** the at least one substantially full-length heterolog with a desired property in an automated or partially automated high-throughput assay system.

. . .

. . . recombining or mutating the at least one substantially full-length heterolog to produce a library of diversified heterologs; and (ii) optionally, **identifying** at least one diversified heterolog with a desired property.

. . . between the alignment; (iii) calculating a melting temperature for one or more window of w bases in the alignment; (iv) **identifying** one or more window of w bases having a melting temperature greater than x; (v) **identifying** one or more crossover segment in the alignment, which one or more crossover segment comprises two or more windows having. . . on the number of windows having a melting temperature grater that x, the dispersion, and the number of crossover segments **identified**; (viii) calculating a second score based on the number of mismatches, the number of windows having a melting temperature grater that x, the dispersion, and the number of crossover segments **identified**; and, (ix) selecting one or more parental nucleic acid based on the first score and/or the second score.

L1 ANSWER 10 OF 11 USPATFULL
AN 2001:183179 USPATFULL
TI Modified ribulose 1,5-bisphosphate carboxylase/oxygenase for improvement and optimization of plant phenotypes
IN Stemmer, Willem P.C., Los Gatos, CA, United States
Subramanian, Venkitswaran, San Diego, CA, United States
Zhu, Genhai, Sunnyvale, CA, United States
Liu, Lu, Redwood City, CA, United States
Selifonov, Sergey A., Los Altos, CA, United States
PA Maxygen. Inc. (U.S. corporation)
PI US 2001032342 A1 20011018
AI US 2001-800123 A1 20010305 (9)
RLI Continuation of Ser. No. US 1999-437726, filed on 9 Nov 1999, PENDING
PRAI US 1999-153093P 19990909 (60)
US 1998-107756P 19981110 (60)
DT Utility
FS APPLICATION
LREP LAW OFFICES OF JONATHAN ALAN QUINE, P O BOX 458, ALAMEDA, CA, 94501
CLMN Number of Claims: 26
ECL Exemplary Claim: 1
DRWN 5 Drawing Page(s)
LN.CNT 3440
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
CLM What is claimed is:
. . . assaying individual or pooled transformants for Rubisco catalytic activity to determine the relative or absolute Km for CO.sub.2 and thereby **identifying** at least one enhanced transformant that expresses a Rubisco activity which has a significantly lower Km for CO.sub.2 than the. . .
. . . comprises assaying individual or pooled transformants for Rubisco catalytic activity to determine the relative or absolute Km for O.sub.2 and **identifying** at least one enhanced transformant that expresses a Rubisco activity which has a significantly higher Km for O.sub.2 than the. . .
. . . or pooled transformants for Rubisco catalytic activity to determine the relative or absolute Km for O.sub.2 and Km for CO.sub.2 **identifying** at least one enhanced transformant that expresses a Rubisco activity which has a significantly lower ratio of Km for CO.sub.2. . .
21. The method of claim 19, wherein the recombining step is performed in vitro, in **silico** or in vivo, or a combination thereof.

L1 ANSWER 11 OF 11 USPATFULL
AN 2001:145506 USPATFULL
TI Generation of virtual combinatorial libraries of compounds
IN Griffey, Richard, Vista, CA, United States
Swayze, Eric, Carlsbad, CA, United States
PA ISIS Pharmaceuticals, Inc. (U.S. corporation)
PI US 2001018645 A1 20010830
AI US 2001-753869 A1 20010103 (9)
RLI Continuation of Ser. No. US 1998-76405, filed on 12 May 1998, GRANTED, Pat. No. US 6253168
DT Utility
FS APPLICATION
LREP Paul K. Legaard, WOODCOCK WASHBURN KURTZ, MACKIEWICZ & NORRIS LLP, One Liberty Place- 46th Floor, Philadelphia, PA, 19103
CLMN Number of Claims: 26
ECL Exemplary Claim: 1
DRWN 20 Drawing Page(s)
LN.CNT 1124
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
CLM What is claimed is:
1. A method of generating a virtual library of compounds in

**silico** comprising: selecting in **silico** a group of related fragments, each of said fragments constituting a part of said compounds, each of said related fragments having at least one attachment site; selecting in **silico** at least one further fragment having at least one attachment site; and linking in **silico** said further fragment to said related fragments by connecting the attachment site of said further fragment to the attachment site. . .

2. A method of generating a virtual library of compounds in **silico** comprising: selecting in **silico** a first fragment, said first fragment constituting a part of said compounds and having at least one attachment site; selecting in **silico** a group of related fragments, each of said group of related fragments having at least one attachment site; and linking in **silico** each of said group of related fragments to said first fragment by connecting the attachment site of each of said. . .

3. A method of generating a virtual library of compounds in **silico** comprising: selecting in **silico** a first group of related fragments, each of said first group of related fragments constituting a part of said compounds and having at least one attachment site; selecting in **silico** a further group of fragments, each of said further group of fragments having at least one attachment site; and linking in **silico** each of said first group of related fragments to each of said further group of fragments by connecting the attachment. . .

4. The method of claim 1 wherein each of said fragments is introduced in **silico** into said compounds by the use a corresponding reagent.

5. The method of claim 2 wherein each of said fragments is introduced in **silico** into said compounds by the use a corresponding reagent.

6. The method of claim 3 wherein each of said fragments is introduced in **silico** into said compounds by the use a corresponding reagent.

7. A method of **identifying** in **silico** each compound of a virtual library of compounds comprising: dissecting said compounds into fragments; and **identifying** each of said fragments in terms of a transformation wherein said transformation is a one to one link between the. . .

9. A method of generating a virtual library of compounds in **silico** comprising: dissecting said compounds into fragments; representing each of said fragments in **silico** as a transformation wherein each transformation is a one to one link between a fragment and a reagent used to introduce said fragment into one of said compounds; selecting in **silico** a first group of said fragments, each of said first group of fragments constituting a part of said compounds, each of said first group fragments having at least one attachment site; selecting in **silico** at least one further fragment having at least one attachment site; and linking in **silico** said further fragment to said first group of fragments by connecting the attachment site of said further fragment to the. . .

10. A method of generating a virtual library of compounds in **silico** comprising: dissecting said compounds into fragments; representing each of said fragments in **silico** as a transformation wherein each transformation is a one to one link between a fragment and a reagent used to introduce said fragment into one of said compounds; selecting in **silico** a fragment, said first fragment constituting a part of said compounds, said first fragment having at least one attachment site; selecting in **silico** at group of further fragments each having at least one attachment site; and linking in **silico** said group of further fragments to said first fragment by connecting the attachment site of said group of further fragments. . .

11. A method of generating a virtual library of compounds in **silico** comprising: dissecting said compounds into fragments;

representing each of said fragments in **silico** as a transformation wherein each transformation is a one to one link between a fragment and a reagent used to introduce said fragment into one of said compounds; selecting in **silico** a first group of said fragments, each of said first group of fragments constituting a part of said compounds, each of said first group fragments having at least one attachment site; selecting in **silico** at group of further fragments each having at least one attachment site; and linking in **silico** at least some of the members of said group of further fragments to least some of members of said first. . .

12. A method of **identifying** in **silico** each compound of a virtual library of compounds comprising: dissecting said compounds into fragments; adding said fragments together in sequential. . .

13. A method of **identifying** in **silico** each compound of a virtual library of compounds comprising: dissecting said compounds into fragments; representing each of said fragments in **silico** as a transformation wherein each transformation is a one to one link between a fragment and a reagent used to. . . introduce said fragment into one of said compounds; adding said transformations together in sequential synthesis rounds; and tracking transformations in **silico**.